

logo

NTDB id 1355 HI 0298 AAC21962.1	MSA	ITTEPKNSGFTPLVQEGLLATIQEQLLLEQVKASKISMEYLLSSQFSTQELTEQSFLGLPDTLQYDYSPLW	27
NTDB id 1366 NTHI RS01950 WP 011271972.1		MTSYA.....LIHTQRVTAKNGE.....VFTISPDLW	27
NTDB id 199689 BG559 RS04635 WP 006251341.1		MTSYA.....LIHTQRVTAQNGE.....IFTISPDLW	21
NTDB id 1384 A4U84 RS08525 WP 010787006.1		MEYS.....V.....TDLNSQR.....FIEISAEQW	22
NTDB id 1168 A1552VC RS11070 WP 000957200.1		MSQYT.....I.....CEQQTER.....TFDISPSRW	72
NTDB id 1401 DSB67 RS12665 WP 010643259.1		MLTNLVAIRLQAELISATQEQAVVTQVSASGTSVPEALLLELSIFHAQELTEQLSHIFGLPETDLSTRDYANL	72
NTDB id 1293 VP RS12240 WP 005479695.1		MLTNLSTVLRQAGILTFQSQEESLLEQVKASGISMPEALLSSGFFQSHETHEHLSSVFGLSCTSLNQYEYASL	72
NTDB id 1251 GC085 RS07725 WP 011946523.1		MHSNLSTILRQKGLLTFQSQEESLLEQVKASGISMPEALLSSGFFTSSSLAEHLSSIFGLSQPELSQYEYASL	80
NTDB id 1018 ACIAD RS01685 WP 004920473.1	MALATEEYRLQGIGQLLVLEKLLDKTKAIELHKLAAAEKISLLQYIVKNKILSAEQIALTAQNFQVPMLDINCLIDVGTI	MSAFTTPPKFSGFIRRLVEEGYVNAQNMQQAIEKAKKFKQDIVPYLIDNFSISPLTIAEITISLEFGEPLLDLGVDPALF	80
NTDB id 1058 ABD1 RS01615 WP 001274986.1	MSALHTSPKFI	IGFFRRLLVEEKHVSAATMQTALDAAKRAKQDVTAVYLIEEVHLSPSLLAETISAEFAEPYFDLDVYDTSQI	80
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NTDB id 1355 HI 0298 AAC21962.1	ERNQQQQS	LLRYFALPLKEENNRLWLGVDSLNLNSACETIAFITGKPVPEILLESSQLKELLQQLTPNQMQVE....EQ	103
NTDB id 1366 NTHI RS01950 WP 011271972.1	ERNQQQQS	LLRYFALPLKEENNRLWLGVDSLNLNSACETIAFITGKPVPEILLESSQLKELLQQLTPHQMQVE....EQ	103
NTDB id 199689 BG559 RS04635 WP 006251341.1	QKNCNEKQ	ILLRYLAVPLQETAEQLWLGIIDDMQNLNACEIFAFIYHKQIEPVLISSEELKFLNLALSPEQSSPQSEIYEE	101
NTDB id 1384 A4U84 RS08525 WP 010787006.1	QKNCNEKQ	ILLRYLAVPVQETEHKLWLAVDDENNLTACEIFAFMTHKQIEPVVIASDELKYLNLALSPEQQ....PIYEE	98
NTDB id 1168 A1552VC RS11070 WP 000957200.1	CQQLGLRELITRYDALPIAKQCNLLLLAVSDPTLLQAEFEFRFATGLQVELALADHRAALQAATIRRLYGRSTIQGAANQGKE	CQTLGLRDLITRHNALPLNRTSSTLILAVADPTNLQAEDDFRATGLQVELVLADFRELTAATIRRLYGRSLGQEKSGLKE	152
NTDB id 1401 DSB67 RS12665 WP 010643259.1	CQQLGLRELITRHNALPLNRTSSTLILAVADPTNLQAEDDFRATGLQVELVLADFRELTAATIRRLYGRSLGQEKSGLKE	CQQLGLRELITRHNALPLHRTPTSTLLAVADPTNQQAEDDFRATGLQVELVLADFRELSTAATIRRLYGRSLGQEKSGLKE	152
NTDB id 1293 VP RS12240 WP 005479695.1	PVNLVNEKLIKRRHAMVPLFSRGTNLVYLATDDPSKQASLKEIQFHTGLNTHAIVVETDKLSALIDNLLTAKESQGLSEYVE	LKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDIAIRFNSKLKVEPIIVEHDKLERLLSEHFVEETHFNFDTE..	160
NTDB id 1018 ACIAD RS01685 WP 004920473.1	LKDKIDEKLIQKYRIMPLVHRGHVLYVATSNPTNIEAMDIAIRFNSKLKVEPIIVEHDKLERLLSEHFVEETHFNFDTE..	PKDLVDQKLILKHRIPLLIQRQILYVATSNPSNIEAIDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFDFNDE..	158
NTDB id 1058 ABD1 RS01615 WP 001274986.1	PKDLVDQKLILKHRIPLLIQRQILYVATSNPSNIEAIDAIRFNSKLLVEPVIVEHHKLEKVLGQHFAEESSFDFNDE..		158
consensus		*** * ***** **!* * !***** * * *! ***** ! ** *	

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NTDB id 1355 HI 0298 AAC21962.1	VKF.....	YQHQETHFEQEDDEPVIRLLNQIFESALQKNASDIHLETADQFQVRFRI	170
NTDB id 1366 NTHI RS01950 WP 011271972.1	VKF.....	YQHQETHFEQEDDEPVIRLLNQIFESALQKNASDIHLETADQFQVRFRI	170
NTDB id 199689 BG559 RS04635 WP 006251341.1	NPL.....	YPFSENTEQPDNDPIITQILENLFKFCLQKNASDIHLEPQKERLLIRLRIDGVLHIYKSLPSSL	168
NTDB id 1384 A4U84 RS08525 WP 010787006.1	SEL.....	AFVEQEQEQLNLNDPIITQLLDNLFKFCLAQNASDIHIEPRKQKLIIRLRIDGVLHLYKSLSIQL	165
NTDB id 1168 A1552VC RS11070 WP 000957200.1	ISQD..	ELANLVKVSDDDELQSIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYENQYRIRLRCDGITLVETQQPASHL	230
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NTDB id 1293 VP RS12240 WP 005479695.1	INQE..	ELASLVVGADIEDNIEDLSQDDSPVSRFINQVLLDAVRKGASDIHFEPYERMYRVRLRCDGITLIETQPPNHL	230
NTDB id 1251 GC085 RS07725 WP 011946523.1	DSGDLEGLEISAD.DEDQDIDTATSVTD	DAPIVKFVNKILLDAIRQGASDIHFEPYERMYRIRYRQDGLHEVATPPASL	239
NTDB id 1018 ACIAD RS01685 WP 004920473.1	.ELD...	LDVEVDPHTTDDDDDDKLKDEAPIVKYINKLLIDAIRMSASDLHFEPYEKSYRVRYRVDGVLRLIATPPLQL	234
NTDB id 1058 ABD1 RS01615 WP 001274986.1	.EFD...	LDVNLGDPTAQDEEEAPQGDEAPIVKYINKLLIDAIRMGASDLHFEPYEKSYRVRYRVDGVLRLQIANPPLQL	234
consensus		* * * * * * * * !***** !!!!!!! * * *	

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consensus

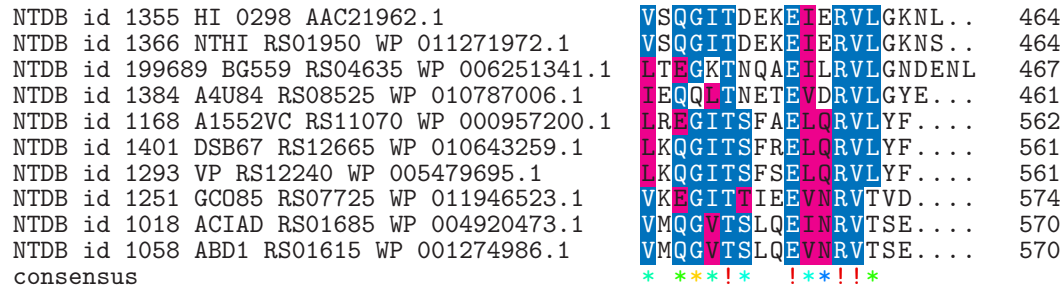
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consensus

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- X non conserved
- X similar
- X $\geq 50\%$ conserved